

SEQUENCE LISTING



A
<110> IKEDA, Joho
SAKAI, Harumi

<120> Monoclonal Antibodies Against Human Apoptosis Inhibitory Protein NAIP,
and Method For Assaying the NAIP

<130> 2001-0515A/WMC/00653

<140> 09/830,338
<141> 2001-04-26

<150> PCT/JP99/05841
<151> 1999-10-22

<160> 2

<210> 1
<211> 1403
<212> PRT
<213> Homo sapiens

<400> 1

Met Ala Thr Gln Gln Lys Ala Ser Asp Glu Arg Ile Ser Gln Phe Asp
1 5 10 15
His Asn Leu Leu Pro Glu Leu Ser Ala Leu Leu Gly Leu Asp Ala Val
20 25 30
Gln Leu Ala Lys Glu Leu Glu Glu Glu Gln Lys Glu Arg Ala Lys
35 40 45
Met Gln Lys Gly Tyr Asn Ser Gln Met Arg Ser Glu Ala Lys Arg Leu
50 55 60
Lys Thr Phe Val Thr Tyr Glu Pro Tyr Ser Ser Trp Ile Pro Gln Glu
65 70 75 80
Met Ala Ala Ala Gly Phe Tyr Phe Thr Gly Val Lys Ser Gly Ile Gln
85 90 95
Cys Phe Cys Cys Ser Leu Ile Leu Phe Gly Ala Gly Leu Thr Arg Leu
100 105 110
Pro Ile Glu Asp His Lys Arg Phe His Pro Asp Cys Gly Phe Leu Leu
115 120 125
Asn Lys Asp Val Gly Asn Ile Ala Lys Tyr Asp Ile Arg Val Lys Asn
130 135 140
Leu Lys Ser Arg Leu Arg Gly Gly Lys Met Arg Tyr Gln Glu Glu
145 150 155 160
Ala Arg Leu Ala Ser Phe Arg Asn Trp Pro Phe Tyr Val Gln Gly Ile
165 170 175
Ser Pro Cys Val Leu Ser Glu Ala Gly Phe Val Phe Thr Gly Lys Gln
180 185 190
Asp Thr Val Gln Cys Phe Ser Cys Gly Gly Cys Leu Gly Asn Trp Glu
195 200 205
Glu Gly Asp Asp Pro Trp Lys Glu His Ala Lys Trp Phe Pro Lys Cys
210 215 220

Glu Phe Leu Arg Ser Lys Lys Ser Ser Glu Glu Ile Thr Gln Tyr Ile
 225 230 235 240
 Gln Ser Tyr Lys Gly Phe Val Asp Ile Thr Gly Glu His Phe Val Asn
 245 250 255
 Ser Trp Val Gln Arg Glu Leu Pro Met Ala Ser Ala Tyr Cys Asn Asp
 260 265 270
 Ser Ile Phe Ala Tyr Glu Glu Leu Arg Leu Asp Ser Phe Lys Asp Trp
 275 280 285
 Pro Arg Glu Ser Ala Val Gly Val Ala Ala Leu Ala Lys Ala Gly Leu
 290 295 300
 Phe Tyr Thr Gly Ile Lys Asp Ile Val Gln Cys Phe Ser Cys Gly Gly
 305 310 315 320
 Cys Leu Glu Lys Trp Gln Glu Gly Asp Asp Pro Leu Asp Asp His Thr
 325 330 335
 Arg Cys Phe Pro Asn Cys Pro Phe Leu Gln Asn Met Lys Ser Ser Ala
 340 345 350
 Glu Val Thr Pro Asp Leu Gln Ser Arg Gly Glu Leu Cys Glu Leu Leu
 355 360 365
 Glu Thr Thr Ser Glu Ser Asn Leu Glu Asp Ser Ile Ala Val Gly Pro
 370 375 380
 Ile Val Pro Glu Met Ala Gln Gly Glu Ala Gln Trp Phe Gln Glu Ala
 385 390 395 400
 Lys Asn Leu Asn Glu Gln Leu Arg Ala Ala Tyr Thr Ser Ala Ser Phe
 405 410 415
 Arg His Met Ser Leu Leu Asp Ile Ser Ser Asp Leu Ala Thr Asp His
 420 425 430
 Leu Leu Gly Cys Asp Leu Ser Ile Ala Ser Lys His Ile Ser Lys Pro
 435 440 445
 Val Gln Glu Pro Leu Val Leu Pro Glu Val Phe Gly Asn Leu Asn Ser
 450 455 460
 Val Met Cys Val Glu Gly Glu Ala Gly Ser Gly Lys Thr Val Leu Leu
 465 470 475 480
 Lys Lys Ile Ala Phe Leu Trp Ala Ser Gly Cys Cys Pro Leu Leu Asn
 485 490 495
 Arg Phe Gln Leu Val Phe Tyr Leu Ser Leu Ser Ser Thr Arg Pro Asp
 500 505 510
 Glu Gly Leu Ala Ser Ile Ile Cys Asp Gln Leu Leu Glu Lys Glu Gly
 515 520 525
 Ser Val Thr Glu Met Cys Met Arg Asn Ile Ile Gln Gln Leu Lys Asn
 530 535 540
 Gln Val Leu Phe Leu Leu Asp Asp Tyr Lys Glu Ile Cys Ser Ile Pro
 545 550 555 560
 Gln Val Ile Gly Lys Leu Ile Gln Lys Asn His Leu Ser Arg Thr Cys
 565 570 575
 Leu Leu Ile Ala Val Arg Thr Asn Arg Ala Arg Asp Ile Arg Arg Tyr
 580 585 590
 Leu Glu Thr Ile Leu Glu Ile Lys Ala Phe Pro Phe Tyr Asn Thr Val
 595 600 605
 Cys Ile Leu Arg Lys Leu Phe Ser His Asn Met Thr Arg Leu Arg Lys
 610 615 620
 Phe Met Val Tyr Phe Gly Lys Asn Gln Ser Leu Gln Lys Ile Gln Lys
 625 630 635 640

卷之三

Thr Pro Leu Phe Val Ala Ala Ile Cys Ala His Trp Phe Gln Tyr Pro
 645 650 655
 Phe Asp Pro Ser Phe Asp Asp Val Ala Val Phe Lys Ser Tyr Met Glu
 660 665 670
 Arg Leu Ser Leu Arg Asn Lys Ala Thr Ala Glu Ile Leu Lys Ala Thr
 675 680 685
 Val Ser Ser Cys Gly Glu Leu Ala Leu Lys Gly Phe Phe Ser Cys Cys
 690 695 700
 Phe Glu Phe Asn Asp Asp Asp Leu Ala Glu Ala Gly Val Asp Glu Asp
 705 710 715 720
 Glu Asp Leu Thr Met Cys Leu Met Ser Lys Phe Thr Ala Gln Arg Leu
 725 730 735
 Arg Pro Phe Tyr Arg Phe Leu Ser Pro Ala Phe Gln Glu Phe Leu Ala
 740 745 750
 Gly Met Arg Leu Ile Glu Leu Leu Asp Ser Asp Arg Gln Glu His Gln
 755 760 765
 Asp Leu Gly Leu Tyr His Leu Lys Gln Ile Asn Ser Pro Met Met Thr
 770 775 780
 Val Ser Ala Tyr Asn Asn Phe Leu Asn Tyr Val Ser Ser Leu Pro Ser
 785 790 795 800
 Thr Lys Ala Gly Pro Lys Ile Val Ser His Leu Leu His Leu Val Asp
 805 810 815
 Asn Lys Glu Ser Leu Glu Asn Ile Ser Glu Asn Asp Asp Tyr Leu Lys
 820 825 830
 His Gln Pro Glu Ile Ser Leu Gln Met Gln Leu Leu Arg Gly Leu Trp
 835 840 845
 Gln Ile Cys Pro Gln Ala Tyr Phe Ser Met Val Ser Glu His Leu Leu
 850 855 860
 Val Leu Ala Leu Lys Thr Ala Tyr Gln Ser Asn Thr Val Ala Ala Cys
 865 870 875 880
 Ser Pro Phe Val Leu Gln Phe Leu Gln Gly Arg Thr Leu Thr Leu Gly
 885 890 895
 Ala Leu Asn Leu Gln Tyr Phe Phe Asp His Pro Glu Ser Leu Ser Leu
 900 905 910
 Leu Arg Ser Ile His Phe Pro Ile Arg Gly Asn Lys Thr Ser Pro Arg
 915 920 925
 Ala His Phe Ser Val Leu Glu Thr Cys Phe Asp Lys Ser Gln Val Pro
 930 935 940
 Thr Ile Asp Gln Asp Tyr Ala Ser Ala Phe Glu Pro Met Asn Glu Trp
 945 950 955 960
 Glu Arg Asn Leu Ala Glu Lys Glu Asp Asn Val Lys Ser Tyr Met Asp
 965 970 975
 Met Gln Arg Arg Ala Ser Pro Asp Leu Ser Thr Gly Tyr Trp Lys Leu
 980 985 990
 Ser Pro Lys Gln Tyr Lys Ile Pro Cys Leu Glu Val Asp Val Asn Asp
 995 1000 1005
 Ile Asp Val Val Gly Gln Asp Met Leu Glu Ile Leu Met Thr Val Phe
 1010 1015 1020
 Ser Ala Ser Gln Arg Ile Glu Leu His Leu Asn His Ser Arg Gly Phe
 1025 1030 1035 1040
 Ile Glu Ser Ile Arg Pro Ala Leu Glu Leu Ser Lys Ala Ser Val Thr
 1045 1050 1055

卷之三

Lys Cys Ser Ile Ser Lys Leu Glu Leu Ser Ala Ala Glu Gln Glu Leu
 1060 1065 1070
 Leu Leu Thr Leu Pro Ser Leu Glu Ser Leu Glu Val Ser Gly Thr Ile
 1075 1080 1085
 Gln Ser Gln Asp Gln Ile Phe Pro Asn Leu Asp Lys Phe Leu Cys Leu
 1090 1095 1100
 Lys Glu Leu Ser Val Asp Leu Glu Gly Asn Ile Asn Val Phe Ser Val
 1105 1110 1115 1120
 Ile Pro Glu Glu Phe Pro Asn Phe His His Met Glu Lys Leu Leu Ile
 1125 1130 1135
 Gln Ile Ser Ala Glu Tyr Asp Pro Ser Lys Leu Val Lys Leu Ile Gln
 1140 1145 1150
 Asn Ser Pro Asn Leu His Val Phe His Leu Lys Cys Asn Phe Phe Ser
 1155 1160 1165
 Asp Phe Gly Ser Leu Met Thr Met Leu Val Ser Cys Lys Lys Leu Thr
 1170 1175 1180
 Glu Ile Lys Phe Ser Asp Ser Phe Phe Gln Ala Val Pro Phe Val Ala
 1185 1190 1195 1200
 Ser Leu Pro Asn Phe Ile Ser Leu Lys Ile Leu Asn Leu Glu Gly Gln
 1205 1210 1215
 Gln Phe Pro Asp Glu Glu Thr Ser Glu Lys Phe Ala Tyr Ile Leu Gly
 1220 1225 1230
 Ser Leu Ser Asn Leu Glu Glu Leu Ile Leu Pro Thr Gly Asp Gly Ile
 1235 1240 1245
 Tyr Arg Val Ala Lys Leu Ile Ile Gln Gln Cys Gln Gln Leu His Cys
 1250 1255 1260
 Leu Arg Val Leu Ser Phe Phe Lys Thr Leu Asn Asp Asp Ser Val Val
 1265 1270 1275 1280
 Glu Ile Ala Lys Val Ala Ile Ser Gly Gly Phe Gln Lys Leu Glu Asn
 1285 1290 1295
 Leu Lys Leu Ser Ile Asn His Lys Ile Thr Glu Glu Gly Tyr Arg Asn
 1300 1305 1310
 Phe Phe Gln Ala Leu Asp Asn Met Pro Asn Leu Gln Glu Leu Asp Ile
 1315 1320 1325
 Ser Arg His Phe Thr Glu Cys Ile Lys Ala Gln Ala Thr Thr Val Lys
 1330 1335 1340
 Ser Leu Ser Gln Cys Val Leu Arg Leu Pro Arg Leu Ile Arg Leu Asn
 1345 1350 1355 1360
 Met Leu Ser Trp Leu Leu Asp Ala Asp Asp Ile Ala Leu Leu Asn Val
 1365 1370 1375
 Met Lys Glu Arg His Pro Gln Ser Lys Tyr Leu Thr Ile Leu Gln Lys
 1380 1385 1390
 Trp Ile Leu Pro Phe Ser Pro Ile Ile Gln Lys
 1395 1400 1403

<210> 2
<211> 5984
<212> DNA
<213> *Homo sapiens*

<220>
<221> CDC

<222> (292)..(4500)

<400> 2

ACAAAAGGTC	CTGTGCTCAC	CTGGGACCCCT	TCTGGACGTT	GCCCCTGTGTT	CCTCTTCGCC	60
TGCCTGTTCA	TCTACGACGA	ACCCCAGGGTA	TTGACCCCCAG	ACAACAATGC	CACTTCATAT	120
TGGGGACTTC	GTCTGGGATT	CCAAGGTGCA	TTCATCGAA	AGTTCCCTAA	ATATTTCTC	180
ACTGCTTCCT	ACTAAAGGAC	GGACAGAGCA	TTTGGTCTTC	AGCCACATAC	TTTCCTTCCA	240
CTGGCCAGCA	TTCTCCTCTA	TTAGACTAGA	ACTGTGGATA	AACCTCAGAA	AATGGCCACC	300
CAGCAGAAAG	CCTCTGACGA	GAGGATCTCC	CAGTTGATC	ACAATTTGCT	GCCAGAGCTG	360
TCTGCTCTTC	TGGGCCTAGA	TGCAGTTCAAG	TTGGCAAAGG	AACTAGAAGA	AGAGGAGCAG	420
AAGGAGCGAG	CAAAAATGCA	GAAAGGCTAC	AACTCTCAA	TGCGCAGTGA	AGCAAAAAGG	480
TTAAAGACTT	TTGTGACTTA	TGAGCCGTAC	AGCTCATGGA	TACCACAGGA	GATGGCGGCC	540
GCTGGGTTTT	ACTTCACTGG	GGTAAAATCT	GGGATTCACT	GCTTCTGCTG	TAGCCTAAC	600
CTCTTGGTG	CCGGCCTCAC	GAGACTCCCC	ATAGAAGACC	ACAAGAGGT	TCATCCAGAT	660
TGTGGGTTCC	TTTGAAACAA	GGATGTTGGT	AACATTGCCA	AGTACGACAT	AAGGGTGAAG	720
AATCTGAAGA	GCAGGCTGAG	AGGAGGTAAA	ATGAGGTACC	AAGAAGAGGA	GGCTAGACTT	780
GCATCCTTCA	GGAACTGGCC	ATTTTATGTC	CAAGGGATAT	CCCCTTGTTG	GCTCTCAGAG	840
GCTGGCTTTG	TCTTACAGG	AAAACAGGAC	ACGGTACAGT	GTTTTCCCTG	TGGTGGATGT	900
TTAGGAAATT	GGGAAGAAGG	AGATGATCCT	TGGAAGGAAC	ATGCCAAATG	GTTCCCCAAA	960
TGTGAATTTC	TTCGGAGTAA	GAAATCCTCA	GAGGAAATT	CCCAGTATAT	TCAAAGCTAC	1020
AAGGGATTTG	TTGACATAAC	GGGAGAACAT	TTTGTGAATT	CCTGGGTCCA	GAGAGAATTA	1080
CCTATGGCAT	CAGCTTATTG	CAATGACAGC	ATCTTGCCT	ACGAAGAACT	ACGGCTGGAC	1140
TCTTTTAAGG	ACTGGCCCCG	GBAATCAGCT	GTGGGAGTTG	CAGCACTGGC	CAAAGCAGGT	1200
CTTTCTACA	CAGGTATAAA	GGACATCGTC	CAGTGCTTT	CCTGTGGAGG	GTGTTAGAG	1260
AAATGGCAGG	AAGGTGATGA	CCCATTAGAC	GATCACACCA	GATGTTTCC	CAATTGTCCA	1320
TTTCTCCAAA	ATATGAAGTC	CTCTGCGGAA	GTGACTCCAG	ACCTTCAGAG	CCGTGGTGAA	1380
CTTGTGAAT	TACTGAAAC	CACAAGTGAA	AGCAATCTTG	AAGATTCAAT	AGCAGTTGGT	1440
CCTATAGTGC	CAGAAATGGC	ACAGGGTGAA	GCCCAGTGGT	TTCAAGAGGC	AAAGAATCTG	1500
AATGAGCAGC	TGAGAGCAGC	TTATACCGAC	GCCAGTTCC	GCCACATGTC	TTTGCTTGAT	1560
ATCTCTTCCG	ATCTGCCAC	GGACCACTTG	CTGGGCTGTG	ATCTGTCTAT	TGCTTCAAAA	1620
CACATCAGCA	AACCTGTGCA	AGAACCTCTG	GTGCTGCCCTG	AGGTCTTGG	CAACTTGAAC	1680
TCTGTATGT	GTGTGGAGGG	TGAAGCTGGA	AGTGGAAAGA	CGGTCCCTCT	GAAGAAAATA	1740
GCTTTCTGT	GGGCATCTGG	ATGCTGTCCC	CTGTAAACAA	GGTCCAGCT	GGTTTCTAC	1800
CTCTCCCTTA	GTTCCACCA	ACCACACGAG	GGGCTGGCCA	GTATCATCTG	TGACCCAGCTC	1860
CTAGAGAAAG	AAGGATCTGT	TACTGAAATG	TGCATGAGGA	ACATTATCCA	GCAGTTAAAG	1920
AATCAGGTCT	TATTCTTTT	AGATGACTAC	AAAGAAATAT	GTTCAATCCC	TCAAGTCATA	1980
GGAAAACGTGA	TTCAAAAAAA	CCACTTATCC	CGGACCTGCC	TATTGATTGC	TGTCCTGTACA	2040
AACAGGGCCA	GGGACATCCG	CCGATACCTA	GAGACCATTG	TAGAGATCAA	AGCATTCCC	2100
TTTATAATA	CTGTCTGTAT	ATTACGGAAG	CTCTTTTCAC	ATAATATGAC	TGCTCTGCCA	2160
AAGTTTATGG	TTTACTTTGG	AAAGAACCAA	AGTTGCGAGA	AGATACAGAA	AACTCCTCTC	2220
TTTGTGGCG	CGATCTGTGC	TCATTGGTTT	CAGTATCCTT	TTGACCCATC	CTTTGATGAT	2280
GTGGCTGTTT	TCAAGTCCTA	TATGGAACGC	CTTCCCTTAA	GGAACAAAGC	GACAGCTGAA	2340
ATTCTCAAAG	CAACTGTGTC	CTCCTGTGGT	GAGCTGGCCT	TGAAAGGGTT	TTTTCATGT	2400
TGCTTGTAGT	TTAATGATGA	TGATCTCGCA	GAAGCAGGGG	TTGATGAAGA	TGAAGATCTA	2460
ACCATGTGCT	TGATGAGCAA	ATTACAGCC	CAGAGACTAA	GACCATTCTA	CCGGTTTTTA	2520
AGTCCTGCCT	TCCAAGAATT	TCTTGGGGGG	ATGAGGCTGA	TTGAACCTCT	GGATTCACT	2580
AGGCAGGAAC	ATCAAGATT	GGGACTGTAT	CATTGAAAC	AAATCAACTC	ACCCATGATG	2640
ACTGTAAGCG	CCTACAAACAA	TTTTTGAAAC	TATGTCCTCA	GCCTCCCTTC	AACAAAAGCA	2700
GGGCCAAAAA	TTGTGTCTCA	TTTGCTCCAT	TTAGTGGATA	ACAAAGAGTC	ATTGGAGAAT	2760
ATATCTGAAA	ATGATGACTA	CTTAAAGCAC	CAGCCAGAAA	TTTCACTGCA	GATGCAGTTA	2820
CTTAGGGGAT	TGTGGCAAAT	TTGTCCACAA	GCTTACTTTT	CAATGGTTTC	AGAACATTAA	2880
CTGGTTCTTG	CCCTGAAAAC	TGCTTATCAA	AGCAACACTG	TTGCTGCGTG	TTCTCCATT	2940

GTTTGCAAT	TCCTTCAAGG	GAGAACACTG	ACTTGGGTG	CGCTTAACCT	ACAGTACTTT	3000
TTCGACCACC	CAGAAAGCTT	GTCATTGTTG	AGGAGCATCC	ACTTCCCAAT	ACGAGGAAAT	3060
AAGACATCAC	CCAGAGCACA	TTTTTCAGTT	CTGGAAACAT	GTTTGACAA	ATCACAGGTG	3120
CCAACTATAG	ATCAGGACTA	TGCTTCTGCC	TTTGAACCTA	TGAATGAATG	GGAGCGAAAT	3180
TTAGCTGAAA	AAGAGGATAA	TGTAAAGAGC	TATATGGATA	TGCAGCGCAG	GGCATCACCA	3240
GACCTTAGTA	CTGGCTATTG	GAAACTTCT	CCAAAGCAGT	ACAAGATTCC	CTGTCTAGAA	3300
GTCGATGTGA	ATGATATTGA	TGTTGTAGGC	CAGGATATGC	TTGAGATTCT	AATGACAGTT	3360
TTCTCAGCTT	CACAGCGCAT	CGAACCTCAT	TTAAACCACA	GCAGAGGCTT	TATAGAAAGC	3420
ATCCGCCAG	CTCTTGAGCT	GTCTAAGGCC	TCTGTCACCA	AGTGCTCCAT	AAGCAAGTTG	3480
GAACTCAGCG	CAGCCGAACA	GBAACTGCTT	CTCACCCCTGC	CTTCCCTGGA	ATCTCTTGAA	3540
GTCTCAGGGA	CAATCCAGTC	ACAAGACCAA	ATCTTCCCTA	ATCTGGATAA	GTTCCTGTGC	3600
CTGAAAGAAC	TGTCTGTGGA	TCTGGAGGGC	AATATAATG	TTTTTCAGT	CATTCCGTGAA	3660
GAATTCCAA	ACTTCCACCA	TATGGAGAAA	TTATTGATCC	AAATTTCAAGC	TGAGTATGAT	3720
CCTTCCAAAC	TAGTAAAATT	AATTCAAAAT	TCTCCAAACC	TTCATGTTT	CCATCTGAAG	3780
TGTAACCTCT	TTTCGATTT	TGGGTCTCTC	ATGACTATGC	TTGTTTCTG	TAAGAAACTC	3840
ACAGAAATTA	AGTTTCGGA	TTCATTTTTT	CAAGCCGTCC	CATTTGTTGC	CAGTTGCCA	3900
AATTTTATT	CTCTGAAGAT	ATTAAATCTT	GAAGGCCAGC	AATTTCTGA	TGAGGAAACA	3960
TCAGAAAAAT	TTGCCTACAT	TTTAGGTCT	CTTAGTAACC	TGGAAGAATT	GATCCCTTCCT	4020
ACTGGGGATG	GAATTATCG	AGTGGCCAAA	CTGATCATCC	AGCAGTGTCA	GCAGCTTCAT	4080
TGTCTCCGAG	TCCTCTCATT	TTTCAAGACT	TTGAATGATG	ACAGCGTGGT	GGAAATTGCC	4140
AAAGTAGCAA	TCAGTGGAGG	TTTCCAGAAA	CTTGAGAAC	TAAGCTTC	AATCAATCAC	4200
AAGATTACAG	AGGAAGGATA	CAGAAATTTC	TTTCAGCAC	TGGACAACAT	GCCAAACTTG	4260
CAGGAGTTGG	ACATCTCCAG	GCATTTCA	GAGTGTATCA	AAGCTCAGGC	CACAAACAGTC	4320
AAGTCTTGA	GTCAATGTGT	GTACGACTA	CCAAGGCTCA	TTAGACTGAA	CATGTTAAGT	4380
TGGCTCTTGG	ATGCAGATGA	TATTGCATG	CTTAATGTCA	TGAAAGAAAG	ACATCCTCAA	4440
TCTAAGTACT	TAACTATTCT	CCAGAAATGG	ATACTGCCGT	TCTCTCCAAT	CATTCAAGAAA	4500
TAAAAGATT	AGCTAAAAAC	TGCTGAATCA	ATAATTGTC	TTGGGGCATA	TTGAGGATGT	4560
AAAAAAAGTT	GTTGATTAAT	GCTAAAAACC	AAATTATCCA	AAATTATTTT	ATTTAAATATT	4620
GCATACAAAA	AAAAATGTGT	AAGGCTTGCT	AAAAACAAA	ACAAAACAAA	ACACAGTCCT	4680
GCATACTCAC	CACCAAGCTC	AAGAAATAAA	TCATCACCAA	TACCTTGTAG	GTCCCTGAGT	4740
AATCCACCCC	AGCTAAAGGC	AAACCCCTCA	ATCAAGTTA	TACAGCAAAC	CCTCCATTGT	4800
CCATGGTCAA	CAGGGAAAGGG	GTTGGGGACA	GGTCTGCCAA	TCTATCTAAA	AGCCACAATA	4860
TGGAAGAAGT	ATTCAATT	TATAATAAT	GGCTTAACCTA	ACGGTTGAAT	CACTTCATA	4920
CATGGATGAA	ACGGGTTAA	CACAGGATCC	ACATGAATCT	TCTGTGGGCC	AAAATATGTT	4980
CCTTAATCCT	TGTAGAACCT	GTCTTCTATA	TTGAACTAGC	TTGGTACAG	TAGAGTTAAC	5040
TTACTTTCCA	TTTATCCACT	GCCAATATAA	AGAGGAAACA	GGGGTTAGGG	AAAAATGACT	5100
TCATTCCAGA	GGCTTCTCAG	AGTTCAACAT	ATGCTATAAT	TTAGAATT	TTATGAATC	5160
CACTCTACTT	GGGTAGAAAA	TATTTTATCT	CTAGTGATTG	CATATTATTT	CCATATCATA	5220
GTATTTCAT	GTATTATATT	TGATATGAGT	GTCTATATCA	ATGTCAGTGT	CCAGAATTTC	5280
GTCCTTACCA	GTTGAGTAGT	TTTCTGAACG	GCCAGAAGAC	CATTGAAAT	TCATGATACT	5340
ACTATAAGT	GGTAAACAAAC	CATACTTTA	TCCTCATTTT	TATTCTCACT	AAGAAAAAAAG	5400
TCAACTCCCC	TCCCCCTGCC	CAAGTATGAA	ATATAGGGAC	AGTATGTATG	GTGTGGTCTC	5460
ATTGTTTAG	AAAACCACTT	ATGACTGGGT	GGGGTGGCTC	ACACCTGTAA	TCCCAGCACT	5520
TTGGGAGGCT	GAGGCGGGCG	AATCATTTGA	GGTGAGGAGT	TCGAGACCGG	CCTGGCCAGC	5580
ATGGTGAAC	CCCATTTTG	CTAAAGGTAC	AAAATTAGC	CAGGTGTGGT	GGCACATGCC	5640
TGTGGTCCCA	GCCACTGGGG	CGGCTGAGAC	GCAGGACTTG	CTTGAACCCG	GGAGGCAGAG	5700
GTTGCAGTGA	GCCGAGATGG	CGCCACTGCA	TTCCAGCTG	GGCAACAGAG	CAAGACCTG	5760
TCTGTTCAA	ACAAAAAAAC	AAAACCACTT	ATATTGCTAG	CTACATTAAG	AATTCTGAA	5820
TATGTTACTG	AGCTTGCTTG	TGGTAACCAT	TTATAATATC	AGAAAGTATA	TGTACACCAA	5880
AACATGTTGA	ACATCCATGT	TGTACAAC	AAATATAAAT	AATTGTCA	ATTATACCTA	5940
AATAAAACTG	AAAAAAAAAA	AAAAAAAAAA	AAAAAAA	AAAA		5984